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Genomics:GTL Awardee Workshop VII and USDA-DOE Plant Feedstock Genomics for Bioenergy Awardee Workshop 2009
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Principal Investigator	Presenter	Title	Poster number	Page number	Session
Scheller, Henrik	Scheller, Henrik	Systematic Characterization of Glycosyltransferases Involved in Plant Cell Wall Biosynthesis	1	3	Monday
Ralph, John	Ralph, John	Streamlined Method For Biomass Whole-Cell-Wall Structural Profiling	1	18	Tuesday
Bartley, Laura	Bartley, Laura	Analysis of Putative Feruloyltransferase Transcript Levels and Cell Wall Composition During Rice Development	2	3	Monday
Markley, John	Fang, Xiaowen	Quantification of Whole Plant Cell Wall and Plant Metabolites Using Advanced 2D 1H-13C HMQC NMR Techniques	2	19	Tuesday
Heazelwood, Joshua	Heazelwood, Joshua	The Utilization of Arabidopsis Genetic Variants to Understand Cell Wall Structure and Biosynthesis	3	4	Monday
Kaeppler, Shawn	Kaeppler, Shawn	Endogenous variation for biofuel quantity and quality traits in maize and switchgrass.	3	20	Tuesday
Vega-Sanchez, Miguel	Vega-Sanchez, Miguel	Selection, Cloning and Functional Characterization of Rice-Diverged, Cell Wall-Related Glycosyltransferases	4	4	Monday
Keegstra, Ken	Keegstra, Ken	Discovery of genes that mediate and regulate hemicellulose biosynthesis	4	20	Tuesday
Yang, Fan	Yang, Fan	Monolignol Transporters and Cell Wall Oxidases Screens	5	5	Monday
Sedbrook, John	Sedbrook, John	Biomass trait screening in a Brachypodium mutant population	5	21	Tuesday
Simmons, Blake	Simmons, Blake	Starting Point for Enzymatic Hydrolysis for Cellulose: Enzyme Engineering of Glycoside Hydrolase-5 Endoglucanases	6	5	Monday
Han, Kyung-Hwan	Han, Kyung-Hwan	Understanding the transcriptional regulation of secondary wall biosynthesis: a step toward optimizing lignocellulosic feedstock for biofuel productivity and processing	6	21	Tuesday
Li, Chenlin	Li, Chenlin	A Comparative Study of Dilute acid and Ionic Liquid Pretreatment of Biomass and Model Lignocellulosics	7	6	Monday
Lipton, Mary	Lipton, Mary	Use of Proteomics Technologies for the Characterization of Proteins, Microbes and Microbial Communities Important for Bioenergy Production	7	22	Tuesday
Singh, Seema	Singh, Seema	Understanding Ionic Liquid Pretreatment of Lignocellulosic Biomasses	8	6	Monday
Fox, Brian	Fox, Brian	Protein Expression Approaches to Cellulose Destruction	8	23	Tuesday
Hazen, Terry	Hazen, Terry	JBEI Microbial Communities Deconstruction Research Activities	9	7	Monday
Phillips, George	Phillips, George	Engineering Cellulases with Improved Stability	9	23	Tuesday

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DeAngelis, Kristen	DeAngelis, Kristen	Discovery And Optimization Of Lignocellulolytic Bacteria From Puerto Rican Rainforest Soils	10	8	Monday
Raines, Ronald	Binder, Joseph	Simple Chemical Transformation of Lignocellulosic Biomass into Fuels and Chemicals	10	23	Tuesday
Allgaier, Martin	Allgaier, Martin	Metagenomic Characterization of Compost and Rain Forest Soil Microbial Communities	11	8	Monday
Keating, David	Keating, David	Construction of a Consolidated Ethanologenic Bioprocessor Derived from Escherichia coli	11	24	Tuesday
Baidoo, Edward	Chhabra, Swapnil	The Fuels Synthesis Division of the Joint BioEnergy	12	9	Monday
Sato, Trey	Sato, Trey	Molecular, Genetic and Genomic Approaches to Alleviate Bottlenecks in Cellulosic Ethanol Production by Yeast	12	24	Tuesday
Chou, Howard	Chou, Howard	Building a de novo Synthetic Metabolic Pathway for Producing Branched-C5 Alcohols	13	9	Monday
Dumesic, James	Braden, Drew	Catalytic Processing of Carbohydrates for the Production of Liquid Fuels	13	25	Tuesday
Dahl, Rob	Dahl, Rob	Transcriptomic Studies of the Response to Exogenous Exposure and Endogenous Production of Biofuel Candidates in E. Coli	14	10	Monday
Pfleger, Brian	Lennen, Rebecca	Engineering E. coli for Production of Hydrocarbons	14	26	Tuesday
Kang, Yisheng	Kang, Yisheng	Increasing Mevalonate Production by Engineering the Metabolism of Escherichia coli	15	10	Monday
Donohue, Timothy	Kontur, Wayne	Networks contributing to photosynthetic biohydrogen production in Rhodobacter sphaeroides	15	26	Tuesday
Lee, Taek Soon	Lee, Taek Soon	Microbial Production of Isoprenoid Biodiesel	16	11	Monday
Tiedje, James	Jesus, Ederson	Bacterial communities in the rhizosphere of biofuel crops as evaluated by 16S rRNA pyrosequencing	16	27	Tuesday
McKee, Adrienne	McKee, Adrienne	Harnessing Genomic Recombination to Improve Microbial Metabolic Phenotypes	17	11	Monday
Thelen, Kurt	Smith, Stephanie	Bio-Energy Cropping Systems on Marginal Land	17	27	Tuesday
Nowroozi, Farnaz	Nowroozi, Farnaz	Optimizing Isoprenoid Biosynthesis	18	128	Monday
Dale, Bruce	Dale, Bruce	Not So Fast Please: New Analysis Gives Much Lower Carbon Debt for Biofuels	18		Tuesday

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Marner, Wesley	Marner, Wesley	Microbial Synthetic Biology at the Great Lakes Bioenergy Research Center: Screening, Fermentation, and Reiterative Engineering	19		Tuesday
Steen, Eric	Steen, Eric	Metabolic Engineering of Saccharomyces Cerevisiae for the Production of n-Butano	19	12	Monday
Noguera, Daniel	Perez, Rodolpho	Using fuel cell-mediated hydrogen conversion in photosynthetic bioreactors	20		Tuesday
Adams, Paul	Mukkhopadhyay, Aindrila	Omics Research at the Joint BioEnergy Institute (JBEI)	20	12	Monday
Chivian, Dylan	Chivian, Dylan	JBEI Computational Biology Core	21	13	Monday
Beers, Eric	Beers, Eric	Towards a map of the Populus biomass protein-protein interaction network	21	44	Tuesday
Hadi, Masood	Hadi, Masood	High Throughput Technologies to Break the Biological Barriers to Cellulosic Fuels	22	13	Monday
Bennetzen, Jeffrey L.	Bennetzen, Jeff	Development of Genomic and Genetic Tools for Foxtail Millet, and Use of These Tools in the Improvement of Biomass Production for Bioenergy Crops	22	45	Tuesday
Northen, Trent	Northen, Trent	High Throughput Mass Spectrometry Based Enzymatic Assays for Biofuels Development	23	14	Monday
Buanafina, Marcia	Buanafina, Marcia	Identifying genes controlling feruloylation in grass cell walls.	23	45	Tuesday
Buckler, Edward	Costich, Denise	Developing association mapping in polyploid perennial biofuel grasses: Establishing the baseline on genome-size variation	24	46	Tuesday
Achyuthan, Komandoor	Achyuthan, Komandoor	Multi-mode Spectroscopic High Throughput Screening (HTS) of Phenols and Monolignols	24	14	Monday
Bharadwaj, Rajiv	Bharadwaj, Rajiv	Microfluidics for Protein Expression, Purification, and Screening	25	16	Monday
Buell, C. Robin and Childs, Kevin L.	Childs, Kevin	Computational Resources for Biofuel Feedstock Species	25	46	Tuesday
Knierim, Bernhard	Knierim, Bernhard	Electron Microscopic Imaging at JBEI	26	16	Monday
Carpita, Nicholas	Carpita, Nicholas	Translational genomics for the improvement of switchgrass	26	47	Tuesday
Petzold, Christopher	Petzold, Christopher	A MRM-based Mass Spectrometry Method for Optimization of Protein Expression to Increase Biofuel Production	27	17	Monday

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Chiang, Vincent	Sun, Ying-Hsuan	Genomic Knowledgebase for Facilitating the Use of Woody Biomass for Fuel Ethanol Production	27	47	Tuesday
Keller, Martin	Davison, Brian	The BioEnergy Science Center - An Overview	28	28	Monday
Dixon, Richard	Dixon, Richard	Systematic modification of monolignol pathway gene expression for improved lignocellulose utilization	28	48	Tuesday
Keller, Martin	Tuskan, Gerald	The Use of TAIL PCR to Identify Genes Controlling Extreme Phenotypes in a Populus Activation Tagged Population	29	28	Monday
Gill, Bikram	Li, Wanlong	Genetic Dissection of the Lignocellulosic Pathway of Wheat to Improve Biomass Quality of Grasses as a Feedstock for Biofuels	29	49	Tuesday
Keller, Martin	Mann, Dave	The pANIC Vector Set for Overexpression of Transgenes and RNAi-Mediated Knockdown of Native Genes in Switchgrass (Panicum virgatum L)	30	29	Monday
Gonzalez, Jose	Gonzalez, Jose	Development of Genomic Tools for the Improvement of Prairie Cordgrass (Spartina pectinata), a Highly Productive Bioenergy Feedstock Crop	30	50	Tuesday
Keller, Martin	Chen, Feng	Genetic modification of lignin biosynthesis in switchgrass	31	30	Monday
Green, Pamela	Gansmann, Matthias	Profiling the small RNAs of Brachypodium distachyon	31	50	Tuesday
Keller, Martin	Pena, Maria	New Insights on the Mechanism of Xylan Biosynthesis	32	30	Monday
Hazen, Samuel	Hazen, Samuel	Transcription factor protein interactions with cell wall gene cis-regulatory regions and their overall role in bioenergy feedstock properties	32	51	Tuesday
Keller, Martin	Yang, Ting	Functional Identification and Characterization of Sugar-1-P Kinases in Arabidopsis	33	31	Monday
Liu, Chang-Jun	Liu, Chang-Jun	Biochemical genomics of wood formation: O-acylesterification for alteration of lignocellulosic property	33	51	Tuesday
Keller, Martin	Hao, Zhangying (Ann)	GAUT12 (GAlactUronosylTransferase 12): A Putative Glycosyltransferase Involved In Arabidopsis Secondary Cell Wall Biosynthesis	34	31	Monday
Liu, Chang-Jun	Gou, Jin-Ying	Characterization of pectin acetylesterase reveals critical roles of cell wall acylesterification in plant growth and development	34	52	Tuesday
Keller, Martin	Elkins, James	Isolation of novel biofuel-relevant thermophiles and the identification of extracellular cellulolytic enzymes using multi-dimensional LC-MS/MS	35	32	Monday
Mockler, Todd	Priest, Henry	Brachypodium Transcriptomics	35	53	Tuesday

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Keller, Martin	Kataeva, Ira	Degradation of Plant Biomass without Pretreatment by the Thermophilic Anaerobe, Anaerocellum thermophilum	36	33	Monday
Peng, Zhaohua	Peng, Zhaohua	Identification of Cell Wall Synthesis Regulatory Genes Controlling Biomass Characteristics and Yield in Rice (Oryza sativa)	36	53	Tuesday
Keller, Martin	Brown, Steven	Integration of genomics and bioinformatics to identify genetic differences in an ethanol tolerant Clostridium thermocellum ATCC27405 strain	37	34	Monday
Bernardo, Rex	Jung, Hans-Joachim	NIRS Prediction of Corn Stover Cell Wall Composition and Conversion Potential, and Relationships among these Traits	37	53	Tuesday
Keller, Martin	Paye, Julie	Advances in Microbial Cellulose Utilization: Methods Development and Kinetics	38	35	Monday
Strauss, Steven	Strauss, Steven	Epigenomics of development in Populus	38	55	Tuesday
Keller, Martin	van der Lelie, Daniel	Metagenomics for mining new deconstructive enzymes, exploring enzyme diversity and screening cellulolytic activities	39	35	Monday
Tobias, Christian	Okada, Miki	A EST-MICROSATELLITE LINKAGE MAP OF SWITCHGRASS (PANICUM VIRGATUM L.) AND COMPARISON WITHIN THE POACEAE	39	55	Tuesday
Keller, Martin	Bomble, Yannick	The Improved Cellulosome: Computational Modeling to Minisomes	40	36	Monday
Chapple, Clint	Ladisch, Michael	Fast Detection of Improved Hydrolysis in Plants with Genetically Modified Lignin	40	56	Tuesday
Keller, Martin	Ziebell, Angela	A rapid analytical pyrolysis method for investigating genetic modification of the lignin pathway in Alfalfa (Medicago sativa)	41	37	Monday
Tuskan, Gerald	Yang, Xiaohan	Genome-enabled Discovery of Carbon Sequestration Genes	41	57	Tuesday
Keller, Martin	Studer, Michael	Integrated High Throughput Pretreatment and Enzymatic Hydrolysis in 96 Well Plates	42	37	Monday
Vermerris, Wilfred	Vermerris, Wilfred	Genetic dissection of bioenergy traits in sorghum	42	58	Tuesday
Keller, Martin	Ding, Shi-You	Advanced Imaging Projects in the BioEnergy Science Center (BESC)	43	38	Monday
Vogel, John	Vogel, John	Insertional Mutagenesis of Brachypodium distachyon	44	58	Tuesday
Leach, Jan	Leach, Jan	Identification of Genes That Control Biomass Production Using Rice as a Model System	43	59	Tuesday
Keller, Martin	Pu, Yunqiao	Analytical BESC Advances in Characterization of Biomass and Recalcitrance	44	39	Monday

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Keller, Martin	Petridis, Loukas	Computer Simulation of Lignocellulosic Biomass	45	40	Monday
DeVos, Katrien	DeVos, Katrien	Resource Development in Switchgrass, a Polyploid Perennial Biofuel Grass.	45	60	Tuesday
Keller, Martin	Yin, Yanbin	The plant cell wall biosynthesis related Galacturonosyltransferase (GAUT) and GAUT like (GATL) genes have a different origin than the other Glycosyltransferase family 8 genes	46	40	Monday
Harrison, Maria	Harrison, Maria	Identification of genes that regulate phosphate acquisition and plant performance during arbuscular mycorrhizal symbiosis in Medicago truncatula and Brachypodium distachyon	46	60	Tuesday
Keller, Martin	Chou, Wen-Chi	Computational Prediction of Golgi Resident Proteins in Arabidopsis thaliana	47	41	Monday
Brummer, Edward	Brummer, Charles	Assessing population genetic structure of diploid alfalfa germplasm as a prelude to association mapping	47		Tuesday
Keller, Martin	Holladay, Susan	The BioEnergy Sciences Center Laboratory Information Management System (LIMS)	48	41	Monday
Keller, Martin	Parang, Morey	The BESC Knowledgebase: An Infrastructure for Biological Discovery	49	42	Monday
Bohn, Paul	Bohn, Paul	Three-Dimensional Spatial Profiling of Lignocellulosic Materials by Coupling Light Scattering and Mass Spectrometry	49	61	Tuesday
Keller, Martin	Doney, Pat	BioEnergy Science Center Education and Outreach	50	43	Monday
Evans, Barbara	Evans, Barbara	Visualization of Acid-Pretreatment Effects on Lignocellulose by Integration of Neutron Scattering and Computer Simulation	50	62	Tuesday
Holman, Hoi-Ying	Holman, Hoi-Ying	Synchrotron Infrared Spectromicroscopy of Cellulose Degradation Strategies of Living Cellulolytic Bacteria	51	63	Tuesday
Beliaev, Alexander	Beliaev, Alexander	Metabolic Modeling for Maximizing Photobiological Hydrogen Production in Cyanobacteria	51	68	Monday
Hammel, Kenneth	Hammel, Kenneth	A NEW SOLUTION-STATE NMR APPROACH TO ELUCIDATE FUNGAL AND ENZYME/MEDIATOR DELIGNIFICATION PATHWAYS	52	64	Tuesday
Dismukes, Charles	Kolling, Derrick	A high-throughput genetic screen for large subunit hydrogenase (hoxH) enzyme presence in Cyanobacteria using whole-cell duplex PCR and novel amplification parameters	52	69	Monday
Hunt, Christopher	Hunt, Christopher	In Vivo Mapping of ROS Produced by Wood Decay Fungi during Early Colonization	53	64	Tuesday

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Dismukes, Charles	Smith, Mark B.	Microalgal Biomass as Feedstock for Production of Hydrogen and Methane Fuel	53	70	Monday
Xie, X. Sunney	Xie, X. Sunney	Stimulated Raman Scattering as an Imaging Tool for Lignocellulosic Biomass Conversion	54	65	Tuesday
Ghirardi, Maria	Ghirardi, Maria	Development of Biologically-Based Assays to Study Rate-Limiting Factors in Algal Hydrogen Photoproduction	54	70	Monday
Thelen, Michael	Lacayo, Catherine	Probing the Architecture of the Plant Cell Wall during Deconstruction in Single Cells from Zinnia elegans	55	65	Tuesday
Gunsalus, Robert	Gunsalus, Robert	Novel hydrogen production systems operative at thermodynamic extremes	55	71	Monday
Peter, Gary	Peter, Gary	Integrated Nondestructive Spatial and Chemical Analysis of Lignocellulosic Materials during Pretreatment and Bioconversion to Ethanol	56	66	Tuesday
Harwood, Caroline	Heiniger, Erin	Mechanism of post-translational control of nitrogenase is revealed by analysis of constitutive hydrogen-producing mutants of Rhodopseudomonas palustris	56	71	Monday
Yang, Haw	Yang, Haw	Single-Molecule Studies of Cellulose Degradation by Celluosomes	57	67	Tuesday
Leigh, John	Leigh, John	Systems Biology of Hydrogen Regulation in Methanococcus maripaludis	57	72	Monday
Meeks, John	Meeks, John	Systems level approaches to understanding and manipulating heterocyst differentiation in Nostoc punctiforme: sites of hydrogenase and nitrogenase synthesis and activity	58	73	Monday
Shimotori, Tsutomu	Shimotori, Tsutomu	Consolidated Bioelectrochemical Processing of Cellulosic Biomass to Ethanol and Hydrogen	58	84	Tuesday
Osterman, Andrei	Osterman, Andrei	Thermotoga maritima Sugar Kinome	59	74	Monday
Blanchard, Jeffrey	Blanchard, Jeffrey	Clostridium phytofermentans: genome sequence of a model system for the direct conversion of plant biomass to fuels	59	85	Tuesday
Osterman, Andrei	Rodionov, Dmitry	Conservation and variations in Shewanella transcriptional regulatory network	60	74	Monday
Blanchard, Jeffrey	Petit, Elsa	A genome-wide perspective on the regulation of plant carbohydrate conversion to biofuels in Clostridium phytofermentans	60	85	Tuesday
Papoyan, Ashot	Papoyan, Ashot	Tetrahymena thermophila as a novel platform for overexpression of membrane and secretory proteins	61		Tuesday

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Pakrisi, Himadri	Pakrasi, Himadri	Development of Cyanothece as a New Model Organism for Biological Hydrogen Production	61	75	Monday
Palsson, Bernhard	Portnoy, Vasiliy	Systems-Level understanding of hydrogen production by Thermotoga maritima	62	76	Monday
Arkin, Adam	Mukhopadhyay, Aindrilla	ESPP Functional Genomics and Imaging Core (FGIC):Cell Wide Analysis of Metal-Reducing Bacteria	62	86	Tuesday
Rabinowitz, Joshua	Amador-Noguez, Daniel	Systems-level kinetic flux profiling elucidates a bifurcated TCA cycle in C. acetobutylicum	63	77	Monday
Arkin, Adam	Bender, Kelly	Analysis of a Desulfovibrio vulgaris Small RNA and Its Target Under Various Stress Conditions	63	87	Tuesday
Scott, Robert	Lipscomb, Gina	Systems Approach to Probing Hydrogen Regulation (SAPHyRe): the SurR redox-switched transcriptional regulator controlling hydrogen production in Pyrococcus furiosus	64	78	Monday
Arkin, Adam	Deutschbauer, Adam	Functional Characterization of Microbial Genomes by Tagged Transposon Mutagenesis	64	87	Tuesday
Seibert, Michael	Seibert, Michael	Filling Knowledge Gaps in Biological Networks: Integrated Global Approaches to Understand H2 Metabolism in Chlamydomonas reinhardtii	65	78	Monday
Arkin, Adam	Kuehl, Jennifer	The development and application of an integrated functional genomics platform in Desulfovibrio desulfuricans G20	65	88	Tuesday
Tabita, F.R.	Laguna, Rick	Examining the molecular basis for the utilization of alternative redox systems to maximize hydrogen production in RubisCO-compromised mutants of nonsulfur purple bacteria	66	80	Monday
Alm, Eric	David, Lawrence	A phylogenomic approach to the evolutionary origins of microbial metabolisms	66	89	Tuesday
Wu, J.H. David	Millen, Jonathan	Pathways and Regulatory Network of Hydrogen Production from Cellulose by Clostridium thermocellum	67	81	Monday
Arkin, Adam	Novichkov, Pavel	Resource for the exploration of regulons accurately predicted by the methods of comparative genomics	67	89	Tuesday
Segre, Daniel	Riehl, William	Inference and integration of regulatory dynamics in metabolic network models	68	81	Monday
Arkin, Adam	Elias, Dwayne	Expression profiling of hypothetical genes in Desulfovibrio vulgaris leads to improved functional annotation	68	90	Tuesday
Wall, Judy	Keller, Kimberly	Effects of mutational modification of electron pathways of Desulfovibrio strains	69	82	Monday

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Arkin, Adam	He, Qiang	Impact of Elevated Nitrate on Sulfate-Reducing Bacteria: Implications of inhibitory mechanisms in addition to osmotic stress	69	90	Tuesday
Noguera, Daniel	Yilmaz, Safak	Modeling electron flow in Rhodobacter sphaeroides for the identification of potential approaches to maximize hydrogen production	70	83	Monday
Arkin, Adam	Rajeev, Lara	A role of CO and a CO sensor protein in the energy metabolism of D. vulgaris Hildenborough	70	91	Tuesday
Arkin, Adam	Zane, Grant	Comparison of the sulfate-reducing capacity of Desulfovibrio vulgaris Hildenborough deleted for the operon containing qmoABC and a hypothetical protein (DVU0851) versus deletion of the hypothetical protein alone	71	91	Tuesday
Fredrickson, Jim	Pinchuk, Grigoriy	CONSTRAINT-BASED METABOLIC MODELING REVEALS HIGH MAINTENANCE ENERGY REQUIREMENT FOR GROWTH OF SHEWNAELLA ONEIDENSIS MR-1 UNDER ELEVATED O2 TENSIONS	71	103	Monday
Arkin, Adam	Zhou, Aifen	The molecular mechanism of adaptation to salt stress revealed by the long-term evolution of Desulfovibrio vugaris Hildenborough	72	92	Tuesday
Lawrence, Charles	McCue, Lee Ann	Phylogenetic footprinting in the Shewanellae	72	103	Monday
Arkin, Adam	He, Zhili	Desulfovibrio vulgaris Hildenborough responses to salt and H2O2 stresses	73	92	Tuesday
Reed, Jennifer	Reed, Jennifer	Constraint-Based Modeling of Metabolism in Shewanella oneidensis MR-1	73	104	Monday
Biggin, Mark	Witkowska, H. Ewa	Analysis of an Intact Dissimilatory Sulfite Reductase Protein Complex from Desulfovibrio vulgaris Using an Ion Mobility QTOF Analyzer	74	93	Tuesday
Romine, Margaret	Romine, Margaret	Progress in Identification of the 'Mobilome' Associated with 21 Sequenced Shewanella sp.	74	105	Monday
Arkin, Adam	Dehal, Paramvir	Microbes Online: an integrated portal for comparative functional genomics	75	94	Tuesday
Saffarini, Daad	Charania, Moiz	Adenylate cyclases and anaerobic respiration in Shewanella oneidensis MR-1	75	106	Monday
Segre, Daniel	Beg, Qasim	Experimental and computational analysis of growth-phase dependent transcriptional programs in Shewanella oneidensis	76	106	Monday
Segre, Daniel	Byrne, David	Metabolic optimality and trade-offs under combinatorial genetic and nutrient modifications	77	107	Monday

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Arkin, Adam	Dubchak, Inna	Progress in the development of the RegTransBase database and the comparative analysis system	78	95	Tuesday
Serres, Margrethe	Serres, Margrethe	Comparative analyses across an evolutionary gradient within the Shewanella genus	78	107	Monday
Hazen, Terry	Hazen, Terry	Applied Environmental Microbiology Core Research on Stress Response Pathways in Metal-Reducers VIMSS:ESPP	79	95	Tuesday
Shanafield, Harold	Shanafield, Harold	EVOLUTION OF SIGNAL TRANSDUCTION IN A BACTERIAL GENUS	79	108	Monday
Arkin, Adam	Singh, Anup	Microfluidic tools for single-cell genomic analysis of environmental bacteria	80	97	Tuesday
Tiedje, James	Auchtung, Jennifer	Investigating environmental specialization in a population of Shewanella baltica strains	80	108	Monday
Arkin, Adam	Van Nostrand, Joy	Applications of GeoChip for analysis of different microbial communities	81	98	Tuesday
Zhou, Jizhong	Liang, Yili	Characterization of C-type Cytochromes and Their Role in Anaerobic Respiration in Shewanella oneidensis and S. putrefaciens	81	109	Monday
Arkin, Adam	Fields, Matthew	Temporal and Spatial Organization within a Syntrophic Bacterial-Archaeal Biofilm	82	99	Tuesday
Zhou, Jizhong	Qiu, Dongru	The NapC- and CymA-Dependent Nitrate Reduction in Shewanella oneidensis MR-1 and S. putrefaciens W3-18-1	82	110	Monday
Arkin, Adam	Hillesland, Kristina	Evolution and Stability in a Syntrophic Community	83	99	Tuesday
Uberbacher, Ed	Uberbacher, Ed	The Shewanella Knowledgebase	83	110	Monday
Spormann, Alfred	Rakshe, Shauna	Control of Shewanella oneidensis MR-1 biofilms by c-di-GMP and environmental factors	84		Monday
Arkin, Adam	Miller, L.D.	Development and Analysis of Multispecies Consortia to Study Microbial Community Stress and Survival	84	100	Tuesday
Arkin, Adam	Fields, Matthew	Characterization of Metal-Reducing Communities and Isolates from Uranium-Contaminated Groundwater and Sediments	85	101	Tuesday
Banfield, Jill	Hettich, Robert	Whole Community Proteomic Approaches to Decipher Protein Information from Natural Microbial Communities	85	130	Monday
Alm, Eric	Alm, Eric	Changing patterns of selection on γ;-proteobacteria revealed by the ratio of substitutions in slow:fast-evolving sites	86	102	Tuesday
Banfield, Jill	Mueller, Ryan	Insights into the ecology and evolution of a natural microbial ecosystem from acid mine drainage using community genomics and proteomics	86	131	Monday

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Alm, Eric	Materna, Arne	Natural Diversity and Experimental Evolution of Environmental Stress Tolerance in Marine Bacteria	87	102	Tuesday
Banfield, Jill	Sun, Christine	Community proteogenomic analysis of virus-host interactions in a natural system	87	132	Monday
Lovley, Derek	Cho, Byung-Kwan	Experimental genome annotation of Geobacter sulfurreducens	88	112	Tuesday
Banfield, Jill	VerBerkmoes, Nathan	Shotgun Proteomics and De-novo Sequencing for the Detection of Viral Signatures in Natural Microbial Communities	88	133	Monday
Lovley, Derek	Franks, Ashley	Novel Approaches for Genome-Scale Spatial Analysis of Gene Transcription in Biofilms: Elucidation of Differences in Metabolism throughout Geobacter sulfurreducens Biofilms Producing High Current Densities	89	112	Tuesday
Breitbart, Mya	Pause, Kimberly	Characterization of viruses from an acid mine drainage system	89	135	Monday
Lovley, Derek	Juarez, Katy	Genome-wide mapping of transcriptional start sites of Geobacter sulfurreducens using high-throughput sequence methodologies	90	114	Tuesday
Doktycz, Michael	Doktycz, Mitchel	Microbially mediated transformation of metal and metal oxide nanoparticles	90	136	Monday
Lovley, Derek	Klimes, Anna	Genome Resequencing Reveals that Current-Harvesting Electrodes Select for Rare Variant of Geobacter sulfurreducens Capable of Enhanced Current Production	91	114	Tuesday
Brodie, Eoin	Brodie, Eoin	Profiling Microbial Identity and Activity: Novel Applications of NanoSIMS and High Density Microarrays	91	137	Monday
Lovley, Derek	Krushkal, Julia	Bioinformatic Analysis of Gene Regulation in Geobacter sulfurreducens: an Integration of Transcriptome and Sequence Information, Molecular Evolutionary Studies, and Database Management	92	116	Tuesday
Weber, Peter	Burow & Woebken	NanoSIP: Functional analysis of phototrophic microbial mat community members using high-resolution secondary ion mass spectrometry	92	138	Monday
Lovley, Derek	Mahadevan, Radhakrishnan	Dynamic Genome-scale Modeling of Geobacter species in Subsurface Environments	93	117	Tuesday
Weber, Peter	Pett-Ridge, Jennifer	NanoSIP: Linking Microbial Phylogeny to Metabolic Activity at the Single Cell Level Using Element Labeling and NanoSIMS Detection	93	138	Monday
Lovley, Derek	Methe, Barbara	The Application of Metagenomic and Metatranscriptomic Approaches to the Study of Microbial Communities in a Uranium-contaminated Subsurface Environment	94	119	Tuesday

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Thelen, Michael	Jiao, Yongqin	Production of Extracellular Polymeric Substances by a Natural Acidophilic Biofilm	94	139	Monday
Lovley, Derek	Risso, Carla	New insights into Rhodoferax ferrireducens through genome annotation and genome-based in silico metabolic modeling	95	120	Tuesday
Kuske, Cheryl	Kuske, Cheryl	Soil Community Metagenomics at the DOE's Climate Change Research Sites	95	140	Monday
Lovley, Derek	Summers, Zarath	Adapative Evolution of Geobacter sulfurreducens under Likely Subsurface Bioremediation Conditions Revealed with Genome Resequencing	96	121	Tuesday
Chisholm, Sallie	Rodrigue, Sebastien	FLOW SORTING AND WHOLE GENOME AMPLIFICATION OF INDIVIDUAL MICROBES	96	141	Monday
Lovley, Derek	Ueki, Toshiyuki	Novel Mechanisms Regulating the Expression of Genes in Geobacter species Important for Metal Reduction, Electricity Production, and Growth in the Subsurface	97	123	Tuesday
Chisholm, Sallie	Thompson, Luke	Viruses Hijacking Cyanobacterial Carbon Metabolism	97	141	Monday
Lovley, Derek	Zengler, Karsten	Nitrogen metabolism in the Geobacteraceae: The role of RpoN	98	124	Tuesday
Chisholm, Sallie	Waldbauer, Jacob	Quantitative Proteomics of Prochlorococcus: Towards an Integrated View of Gene Expression and Cellular Stoichiometry	98	142	Monday
Schiffer, Marianne	Pokkuluri, Raj	Structures and redox potentials of periplasmic cytochromes from Geobacter sulfurreducens	99	125	Tuesday
DeLong, Edward	McCarren, Jay	Bacterioplankton Community Transcriptional Response to Environmental Perturbations	99	142	Monday
McAdams, Harley	Moussavi, Farshid	Automatic Segmentation and Structural Study of the Bacterial Cell Wall in Cryo-Electron Tomography	100	126	Tuesday
Pakrisi, Himadri	Liberton, Michelle	Grand Challenge in Membrane Biology: A systems biology study of the unicellular diazotrophic cyanobacterium Cyanothece sp. ATCC 51142	100	143	Monday
McAdams, Harley	Shapiro, Lucy	Control Mechanisms For Chromosome Orientation and Dynamics in Caulobacter crescentus	101	127	Tuesday
Lidstrom, Mary	Konopka, Michael	Coupling Function to Phylogeny via Single-Cell Phenotyping	101	145	Monday
Ellisman, Mark	Gaietta, Guido	Optimizing the detection of specific protein complexes in Caulobacter crescentus at the electron microscopic level	102	128	Tuesday
Lipton, Mary	Lipton, Mary	Proteomics Driven Analysis of Microbes, Plants and Microbial Communities	102	147	Monday

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Smith, Richard	Anderson, Gordon	High Throughput Comprehensive Quantitative Proteomics and Metabolomics for Genomics:GtL	103	148	Monday
Larabell, Carolyn	McDermott, Gerry	Soft X-ray Tomography: A New Tool for Imaging Prokaryotic Cells	104		Tuesday
Smith, Richard	Smith, Richard	A New Platform for Much Higher Throughput Comprehensive Quantitative Proetomics	104	149	Monday
Larabell, Carolyn	Larabell, Carolyn	Isotropic Soft X-ray Tomography of Eukaryotic Cells	105		Tuesday
Squire, Thomas	Squier, Thomas	Live-Cell Visualization of Tagged Bacterial Protein Dynamics and Turnover	105	150	Monday
Cannon, William	Cannon, William	An Approach to identifying Proteins from Microbial Communities	106		Monday
Larabell, Carolyn	LeGros, Mark	A New Multi-Modal Imaging Technology: High Numerical Aperture Cryogenic Light Microscopy with Correlated Soft X-ray Tomography	106		Tuesday
Maranas, Costas	Ranganathan, Sridhar	Identification of All Engineering Interventions Leading to Targeted Overproductions	107	151	Tuesday
Baker, Scott	Baker, Scott	Toward a high throughput functional annotation pipeline for fungal glycoside hydrolases	107	167	Monday
Maranas, Costas	Suthers, Patrick	Automated construction of genome-scale metabolic models: application to Mycoplasma genitalium	108	152	Tuesday
Church, George	Tolonen, Andrew	Annotation of the Clostridium phytofermentans ORFome by proteogenomic mapping	108	167	Monday
Maranas, Costas	Zomorrodi, Alireza	Synthetic lethality analysis based on the Escherichia coli metabolic model	109	152	Tuesday
Collart, Frank	Frank, Ashley	Protein Functional Assignment Using a Fluorescence-Based Thermal Shift Assay	109	168	Monday
Eisenberg, David	Merchant, Sabeeha; Matteo Pellegrini	Functional analysis of trace nutrient homeostasis in Chlamydomonas using next generation sequencers	110	144	Tuesday
Collart, Frank	Landorf, Elizabeth	Assignment of Enzymatic Function for Core Metabolic Enzymes	110	168	Monday
Konstantinidis, Konstantinos	Konstantinidis, Konstantinos	Whole-genome comparative analyses across an environmental gradient reveal surprisingly rapid bacterial adaptation mediated by horizontal gene transfer	111	144	Tuesday
Cottingham, Robert	Land, Miriam	Quality Improvement Process for JGI-ORNL Microbial Annotation Pipeline	111	169	Monday

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Tainer, John	Tainer, John	High throughput structural characterization of protein complexes in solution using Small Angle X-ray Scattering (SAXS) Combined with Mass Spectrometry (MS)	113	153	Tuesday
de Crecy-Legard, Valerie	El Yacoubi, Basma	Comparative genomics and experimental validation to find universal, globally missing genes: the universal families COG009 and CO0533	113	171	Monday
Adams, Michael W.W.	Cvetkovic, Aleksandar	Define the Metalloproteome by Letting Metals Take the Lead: A Component of the MAGGIE Project	114	154	Tuesday
de Crecy-Legard, Valerie	Pribat, Anne	Genome annotation: Coupling the power of plant-prokaryote comparative genomics to experimental validation, COG0720 and COG3404	114	172	Monday
Yannone, Steven	Yannone, Steven	The MAGGIE Project: Production and Isolation of Native and Recombinant Multiprotein Complexes and Modified Proteins from Hyperthermophilic Sulfolobus solfataricus	115	155	Tuesday
Kent, Stephen	Kent, Stephen	Use of modern chemical protein synthesis techniques to experimentally validate the functional annotation of microbial genomes	115	174	Monday
Baliga, Nitin	Pang, Wyming	Technologies for robust and rational reengineering of microbial systems	116	155	Tuesday
Land, Miriam	Chang, Yun-juan	Towards annotation of the unannotated --- a dissection of unannotated proteins in Clostridium thermocellum	116	175	Monday
Baliga, Nitin	Reiss, David	Dynamic assembly of functional transcriptional complexes inside genes and operons	117	156	Tuesday
Orban, John	Orban, John	An integrated approach to experimental validation of putative gene functions in M. acetivorans	117	175	Monday
Tainer, John	Hura, Greg	Developed proteomics scale solution X-ray scattering (SAXS) tools applied to metabolic networks of interest from the MAGGIE program project	118		Tuesday
Pellegrini, Matteo	Pellegrini, Matteo	Transcriptome analysis of Chlamydomonas Reinhardtii using ultra-high-throughput sequencing	118	176	Monday
Biggin, Mark	Arbelaez, Pablo	Protein Complex Analysis Project (PCAP): Automated Particle Picking in Electron Microscopy Images	119	156	Tuesday

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Biggin, Mark	Butland, Gareth	A high throughput pipeline for identifying protein-protein interactions in Desulfovibrio vulgaris using tandem-affinity purification.	120	157	Tuesday
Siuzdak, Gary	Northen, Trent	Genemap-MS: high throughput mass spectrometry approaches to microbial gene annotation validation	120	178	Monday
Biggin, Mark	Dong, Ming	Protein Complex Analysis Project (PCAP): Protein Complex Purification and Identification by ”Tagless” Strategy	121	157	Tuesday
Siuzdak, Gary	Trauger, Sunia	Novel Mass Spectrometry Based Platforms for the Investigation of Model Organisms	121	178	Monday
Biggin, Mark	Auer, Manfred	Protein Complex Analysis Project (PCAP): Localization of Multi-Protein Complexes through SNAP-Tag Labeling	122	158	Tuesday
Land, Miriam	Hauser, Loren	Annotation of Translation Initiation Sites Using Prodigal	122	179	Monday
Biggin, Mark	Han, Bong-Gyoon	Protein Complex Analysis Project (PCAP): Survey of Large Protein Complexes in Desulfovibrio vulgaris Reveals Unexpected Structural Diversity	123	159	Tuesday
Mansfield, Betty	Mansfield, Betty	Genome Management Information System: A Multifaceted Approach to DOE Systems Biology Research Communication and Facilitation	123	187	Monday
Scott, Bari	Scott, Bari	The DNA Files	124		Monday
Biggin, Mark	Liu, Haichuan	Protein Complex Analysis Project (PCAP): Introduction of Iterative MS/MS Acquisition (IMMA) to the MALDI LC MS/MS Workflow To Enable High Throughput Protein Complex Identification using Tagless Strategy	124	159	Tuesday
Biggin, Mark	Walian, Peter	Protein Complex Analysis Project (PCAP): Isolation and Identification of Membrane Protein Complexes from D. vulgaris	125	160	Tuesday
Scott, Bari	Scott, Bari	Science Literacy Training for Public Radio Journalists	125		Monday
Biggin, Mark	Shatsky, Maxim	Protein Complex Analysis Project (PCAP): Reconstruction of Multiple Structural Conformations of Macromolecular Complexes Studied by Single-Particle Electron Microscopy	126	161	Tuesday
Bennett, Alan	Clark, Kerri	Intellectual property and U.S. public investments in research on biofuel technologies	126	189	Monday

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Bjornstad, David	Bjornstad, David	Implications of Alternative Intellectual Property Rights Management Approaches	127	189	Monday
Downing, Kenneth	Ball, David	PCAP: Towards Localization of Functionality in Desulfovibrio vulgaris by Electron Microscopy	128	162	Tuesday
Selfa, Theresa	Selfa, Theresa	The Biofuels Revolution: Understanding the Social, Cultural, and Economic Impacts of Biofuels Development on Rural Communities	128	190	Monday
Hazen, Terry	Hazen, Terry	Protein Complex Analysis Project (PCAP): High Throughput Identification and Structural Characterization of Multi-Protein Complexes During Stress Response in Desulfovibrio vulgaris: Microbiology Subproject	129	163	Tuesday
Tyner, Wallace	Taheripour, Farzad	Analysis of Global Economic and Environmental Impacts of a Substantial Increase in Bioenergy Production	129	191	Monday
Buchanan, Michelle	Cannon, William	An Integrative Strategy for the Determination of the Modular Structure of Functional Networks of Rhodopseudomonas palustris	130	164	Tuesday
Wolfe, Amy	Wolfe, Amy	Issues associated with the transition from science to application in a fundamental nanoscience user center	130	192	Monday
Zhuang, Qianlai	Lu, Yanyu	Global net primary production and bioenergy potentials and the environmental consequences: An analysis with a process-based terrestrial ecosystem model	131	193	Monday
Buchanan, Michelle	Morrell-Falvey, Jennifer	An Imaging-Based Assay with High Sensitivity for Confirming and Characterizing Protein Interactions	131	165	Tuesday
Anderson, David	Bailey, Vanessa	Agricultural Considerations in Region Selection for Biofuel Economic Impact Modeling	132		Monday
Buchanan, Michelle	Chongle, Pan	Functional Characterization of Protein Complexes and Cellular Systems in Rhodopseudomonas palustris using Stable Isotopic Labeling and Quantitative Proteomics	132	165	Tuesday
Khanna, Madhu	Huang, Haixiao	Meeting the Demand for Biofuels: Impact on Land Use and Carbon Mitigation	133		Monday
Buchanan, Michelle	Pelletier, Dale	Protein-Protein Interactions in Rhodopseudomonas palustris at the Genomics:GTL Center for Molecular and Cellular Systems	133	166	Tuesday

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Garrity, George	Garrity, George	NamesforLife Semantic Resolution Services for the Life Sciences	135	182	Tuesday
Dismukes, Charles	Skizim, Nicholas	Probing the interdependence of hydrogenase- and nitrogenase-dependent hydrogen production in Cyanothece sp. Miami BG043511 by genetic deletion and mutant analysis	135	69	Monday
Garrity, George	Harrison, Scott	Standards in Genomic Sciences: an Open-Access, Standards-Supportive Publication that Rapidly Disseminates Concise Genome and Metagenome Reports in Compliance with MIGS/MIMS Standards	136	183	Tuesday
Joachimiak	Andrzej	Targeting Bioenergy, Environment and New Protein Families: Community Nominated JGI/MCSG Structural Genomics Pilot Project	136		Monday
Tiedje, James	Cole, James	The Ribosomal Database Project: Tools and Sequences for rRNA Analysis	137	184	Tuesday